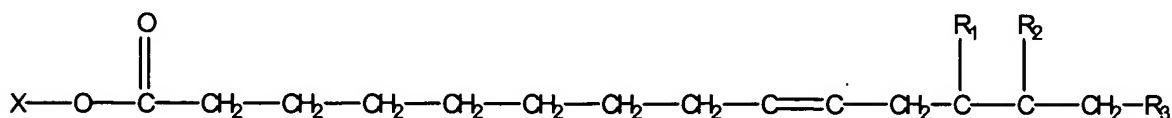


**WHAT IS CLAIMED IS:**

1. A transgenic plant containing at least one DNA construct, said construct comprising:

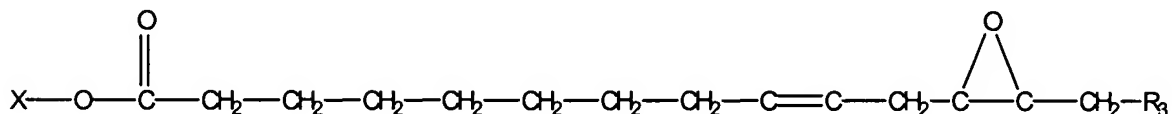
a) a nucleic acid encoding a polypeptide effective for catalysing the conversion of a substrate to a C16, C18, or C20 monounsaturated fatty acid product selected from the group consisting of:

i)



wherein X is hydrogen, CoA, glycerol, a monoglyceride, a diglyceride, ACP, methyl, Na<sup>+</sup>, phosphatidylcholine, or phosphatidylethanolamine, wherein both R<sub>1</sub> and R<sub>2</sub> are hydroxyl, one of R<sub>1</sub> and R<sub>2</sub> is hydroxyl and the other is hydrogen, or one of R<sub>1</sub> and R<sub>2</sub> is keto and the other is hydrogen, and wherein R<sub>3</sub> is C2, C4, or C6 alkyl; and

ii)



wherein X is hydrogen, CoA, glycerol, a monoglyceride, a diglyceride, ACP, methyl, Na<sup>+</sup>, phosphatidylcholine, or phosphatidylethanolamine, and wherein R<sub>3</sub> is C2, C4, or C6 alkyl; and

(b) a regulatory element operably linked to said nucleic acid encoding said polypeptide, wherein said regulatory element confers expression in a vegetative tissue of said plant.

2. The plant according to claim 1, wherein the double bond between the 9<sup>th</sup> and 10<sup>th</sup> carbons is *cis*.

3. The plant according to claim 1, wherein the double bond between the 9<sup>th</sup> and 10<sup>th</sup> carbons is *trans*.
4. The plant according to claim 1, wherein said regulatory element is a 5'-regulatory element.
5. The plant of claim 4, wherein said 5'-regulatory element confers expression in root tissue.
6. The plant of claim 5, said plant having a significantly increased amount of a hydroxy-fatty acid in roots of said plant relative to a corresponding plant that lacks said DNA construct.
7. The plant of claim 6, wherein said hydroxy-fatty acid is ricinoleic acid.
8. The plant of claim 7, wherein said ricinoleic acid constitutes from about 0.1% to about 25% of the total fatty acid content of said roots.
9. The plant of claim 5, said plant having a significantly increased amount of an epoxy-fatty acid in roots of said plant relative to a corresponding plant that lacks said DNA construct.
10. The plant of claim 9, wherein said epoxy-fatty acid is vernolic acid.
11. The plant of claim 10, wherein said vernolic acid constitutes from about 0.1% to about 35% of the total fatty acid content of said roots.
12. The plant of claim 4, wherein said 5'-regulatory element is selected from the group consisting of a CaMV35S promoter, a potato ribosomal protein S27a Ubi3 promoter, a RB7 promoter, an alfalfa histone H3.2 promoter, an IRT2 promoter, an *Arabidopsis* FAD2

5'-UTR, an *Arabidopsis* FAD3 5'-UTR, a Ubi3 5'-UTR, an alfalfa histone H3.2 5'-UTR, and a CaMV35S 5'-UTR.

13. The plant of claim 1, wherein said regulatory element comprises a first 5'-regulatory element operably linked to a second 5'-regulatory element, wherein said first 5'-regulatory element is an Ubi3 promoter and said second 5'-regulatory element is selected from the group consisting of an *Arabidopsis* FAD2 5'-UTR, an *Arabidopsis* FAD3 5'-UTR, a potato ribosomal protein S27a 5'-UTR, a Ubi3 5'-UTR, and a CaMV35S 5'-UTR.

14. The plant of claim 4, wherein said DNA construct further comprises a 3'-regulatory element.

15. The plant of claim 14, wherein said 3'-regulatory element comprises a Ubi3 terminator or an E9 pea terminator.

16. The plant of claim 14, wherein said 5'-regulatory element is selected from the group consisting of an *Arabidopsis* FAD2 5'-UTR and an *Arabidopsis* FAD3 5'-UTR and said 3'-regulatory element is selected from the group consisting of an *Arabidopsis* FAD2 3'-UTR and an *Arabidopsis* FAD3 3'-UTR.

17. The plant of claim 16, wherein said 5'-regulatory element comprises SEQ ID NOS: 43 or 44 and said 3'-regulatory element comprises SEQ ID NO: 45.

18. The plant of claim 1, wherein said at least one DNA construct further comprises at least one regulatory element that confers expression in vegetative tissues of a plant operably linked to a nucleic acid that encodes a PDAT or DAGAT polypeptide.

19. The plant of claim 1, said plant further comprising a second DNA construct, said second DNA construct comprising at least one regulatory element that confers expression in vegetative tissues of a plant operably linked to a nucleic acid that encodes a PDAT or DAGAT polypeptide.

20. The plant of claim 1, wherein R<sub>3</sub> is C2 alkyl or C4 alkyl.
21. The plant of claim 1, wherein said polypeptide is selected from the group consisting of: SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, *C. palaestina* epoxxygenase GenBank® No. CAA76156, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41 and SEQ ID NO: 42.
22. The plant of claim 21, wherein said polypeptide comprises SEQ ID NO: 37.
23. The plant of claim 21, wherein said polypeptide comprises SEQ ID NO: 38.
24. The plant of claim 21, wherein said polypeptide comprises SEQ ID NO: 14.
25. The plant of claim 21, wherein said polypeptide comprises SEQ ID NO: 15.
26. The plant of claim 21, wherein said polypeptide comprises SEQ ID NO: 16.
27. The plant of claim 21, wherein said polypeptide comprises SEQ ID NO: 40.
28. The plant of claim 21, wherein said polypeptide comprises SEQ ID NO: 41.
29. The plant of claim 21, wherein said nucleic acid encoding said polypeptide comprises GenBank® Accession No. CAA76156.
30. The plant of claim 21, wherein said polypeptide comprises SEQ ID NO: 34.
31. The plant of claim 21, wherein said polypeptide comprises SEQ ID NO: 35.

32. The plant of claim 22, wherein said nucleic acid encoding said polypeptide is SEQ ID NO: 28.

33. The plant of claim 23, wherein said nucleic acid encoding said polypeptide is SEQ ID NO: 29.

34. The plant of claim 24, wherein said nucleic acid encoding said polypeptide is SEQ ID NO: 2.

35. The plant of claim 25, wherein said nucleic acid encoding said polypeptide is SEQ ID NO: 3.

36. The plant of claim 26, wherein said nucleic acid encoding said polypeptide is SEQ ID NO: 4.

37. The plant of claim 27, wherein said nucleic acid encoding said polypeptide is SEQ ID NO: 31.

38. The plant of claim 28, wherein said nucleic acid encoding said polypeptide is SEQ ID NO: 32.

39. The plant of claim 30, wherein said nucleic acid encoding said polypeptide is SEQ ID NO: 25.

40. The plant of claim 31, wherein said nucleic acid encoding said polypeptide is SEQ ID NO: 26.

41. The plant of claim 1, wherein said polypeptide is selected from the group consisting of: SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, and a *C. palaestina* epoxygenase chimera.

42. The plant of claim 41, wherein said polypeptide is SEQ ID NO: 19.
43. The plant of claim 41, wherein said polypeptide is SEQ ID NO: 20.
44. The plant of claim 41, wherein said polypeptide is SEQ ID NO: 21.
45. The plant of claim 41, wherein said polypeptide is SEQ ID NO: 22.
46. The plant of claim 41, wherein said polypeptide is SEQ ID NO: 23.
47. The plant of claim 41, wherein said polypeptide is SEQ ID NO: 24.
48. The plant of claim 42, wherein said nucleic acid encoding said polypeptide is SEQ ID NO: 7.
49. The plant of claim 43, wherein said nucleic acid encoding said polypeptide is SEQ ID NO: 8.
50. The plant of claim 44, wherein said nucleic acid encoding said polypeptide is SEQ ID NO: 9.
51. The plant of claim 45, wherein said nucleic acid encoding said polypeptide is SEQ ID NO: 10.
52. The plant of claim 46, wherein said nucleic acid encoding said polypeptide is SEQ ID NO: 11.
53. The plant of claim 47, wherein said nucleic acid encoding said polypeptide is SEQ ID NO: 12.

54. The plant of claim 1, where said plant is selected from the group consisting of tobacco, tomato, soybean, corn, cotton, rice, wheat, banana, carrot, potato, strawberry and turf grass.

55. A method of making a transgenic plant, said method comprising introducing the construct of claim 1 into a plant.

56. The method of claim 55, wherein said regulatory element of said construct is a 5'-regulatory element.

57. The method of claim 56, wherein said 5'-regulatory element comprises a CaMV35S promoter, a potato ribosomal protein S27a Ubi3 promoter, a RB7 promoter, an alfalfa histone H3.2 promoter, an IRT2 promoter, an *Arabidopsis* FAD2 5'-UTR, an *Arabidopsis* FAD3 5'-UTR, a Ubi3 5'-UTR, an alfalfa histone H3.2 5'-UTR, and a CaMV35S 5'-UTR.

58. The method of claim 56, wherein said regulatory element comprises a first 5'-regulatory element operably linked to a second 5'-regulatory element, wherein said first 5'-regulatory element is an Ubi3 promoter and said second 5'-regulatory element is selected from the group consisting of an *Arabidopsis* FAD2 5'-UTR, an *Arabidopsis* FAD3 5'-UTR, a potato ribosomal protein S27a 5'-UTR, a Ubi3 5'-UTR, and a CaMV35S 5'-UTR.

59. The method of claim 56, wherein said DNA construct further comprises a 3'-regulatory element.

60. The method of claim 59, wherein said 5'-regulatory element comprises SEQ ID NO: 43 or SEQ ID NO: 44 and said 3'-UTR comprises SEQ ID NO: 45.

61. The method of claim 55, wherein said nucleic acid of said DNA construct encodes a polypeptide selected from the group consisting of: SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19,

SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, *C. palaestina* epoxxygenase GenBank® No. CAA76156, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41 and SEQ ID NO: 42.

62. The method of claim 55, wherein said polypeptide comprises SEQ ID NO: 13.
63. The method of claim 55, wherein said polypeptide comprises SEQ ID NO: 19.
64. The method of claim 55, wherein said polypeptide comprises SEQ ID NO: 20.
65. The method of claim 55, wherein said polypeptide comprises SEQ ID NO: 21.
66. The method of claim 55, wherein said polypeptide comprises SEQ ID NO: 22.
67. The method of claim 55, wherein said polypeptide comprises SEQ ID NO: 23.
68. The method of claim 55, wherein said polypeptide comprises SEQ ID NO: 24.
69. The method of claim 55, wherein said polypeptide comprises SEQ ID NO: 36.
70. The method of claim 55, wherein said polypeptide comprises SEQ ID NO: 37.
71. The method of claim 55, wherein said polypeptide comprises SEQ ID NO: 38.
72. The method of claim 55, wherein said polypeptide comprises SEQ ID NO: 40.
73. The method of claim 55, wherein said polypeptide comprises SEQ ID NO: 41.
74. An isolated nucleic acid comprising the nucleotide sequence set forth in any one of SEQ ID NOS: 3 to 12 or 25 to 33.



75. The isolated nucleic acid of claim 74, wherein said nucleotide sequence is SEQ ID NO: 3.

76. The isolated nucleic acid of claim 74, wherein said nucleotide sequence is SEQ ID NO: 4.

77. The isolated nucleic acid of claim 74, wherein said nucleotide sequence is SEQ ID NO: 5.

78. The isolated nucleic acid of claim 74, wherein said nucleotide sequence is SEQ ID NO: 28.

79. A recombinant nucleic acid construct comprising at least one regulatory element that confers expression in a vegetative tissue of a plant, said regulatory element operably linked to a nucleic acid having the nucleotide sequence set forth in any one of SEQ ID NOS: 3 to 12 or 25 to 33.

80. The nucleic acid construct of claim 79, wherein said at least one regulatory element comprises a 5'-regulatory element having the nucleotide sequence set forth in SEQ ID NO: 43 or SEQ ID NO: 44.

81. The nucleic acid construct of claim 80, wherein said construct further comprises a 3'-regulatory element having the nucleotide sequence set forth in SEQ ID NO: 45.

82. A method of screening a transgenic plant for anthelmintic activity, comprising contacting the transgenic plant of claim 1 with a plurality of nematodes under conditions effective to determine whether or not said plant has anthelmintic activity.

83. The method of claim 82, wherein said nematodes are contacted with one or more roots of said transgenic plant.

84. A method of screening a transgenic plant for anthelmintic activity, comprising contacting tissue from the transgenic plant of claim 1 with a plurality of nematodes under conditions effective to determine whether or not said plant tissue has anthelmintic activity.

85. The method of claim 84, wherein said tissue is root tissue.

86. A transgenic plant harboring a DNA construct comprising a nucleic acid encoding a fatty acid epoxygenase polypeptide or a fatty acid hydroxylase polypeptide operably linked to a regulatory element conferring expression of said polypeptide in a vegetative tissue of said plant.

87. The plant of claim 86 wherein said polypeptide comprises an amino acid sequence selected from the group consisting of: SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, *C. palaestina* epoxygenase (GenBank® No. CAA76156), SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, and SEQ ID NO: 42.

88. The plant of claim 86, said plant having a significantly increased amount of a hydroxy-fatty acid in roots of said plant relative to a corresponding plant that lacks said DNA construct.

89. The plant of claim 88, wherein said hydroxy-fatty acid is ricinoleic acid.

90. The plant of claim 89, wherein said ricinoleic acid constitutes from about 0.1% to about 25% of the total fatty acid content of said roots.

91. The plant of claim 86, said plant having a significantly increased amount of a epoxy-fatty acid in roots of said plant relative to a corresponding plant that lacks said DNA construct.

92. The plant of claim 91, wherein said epoxy-fatty acid is vernolic acid.

93. The plant of claim 92, wherein said vernolic acid constitutes from about 0.1% to about 35% of the total fatty acid content of said roots.